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<p>Substitute for form 1449A/PTO</p> <p>INFORMATION DISCLOSURE STATEMENT BY APPLICANT</p> <p><i>(Use as many sheets as necessary)</i></p>				Complete if Known	
Application Number		10/032,281			
Filing Date		December 21, 2001			
First Named Inventor		WYRICK, JOHN			
Art Unit		1637			
Examiner Name		Horlick, Kenneth R			
Sheet	1	of	3	Attorney Docket Number	
WTHD-007CIP					

U.S. PATENT DOCUMENTS

FOREIGN PATENT DOCUMENTS

Examiner Signature	/Kenneth Horlick/	Date Considered	05/19/2008
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				Filing Date	December 21, 2001
				First Named Inventor	WYRICK, JOHN
				Art Unit	1637
				Examiner Name	Horlick, Kenneth R
Sheet	2	of	3	Attorney Docket Number	WTHD-007CIP

NON PATENT LITERATURE DOCUMENTS					
Examiner Initials*	Cite No. ¹	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.			T ²
/KH/		BARNARD, et al. PCR bias toward the wild-type k-ras and p53 sequences: Implications for PCR detection of mutations and cancer diagnosis. BioTechniques. 1998, vol. 25, no. 4, pp 684-691.			
		BECKER, et al. PCR bias in ecological analysis: a case study for quantitative Taq nuclease assays in analyses of microbial communities. Applied and Environmental Microbiology. 2004, vol. 66, no. 11, pp. 4945-4953.			
		JI, et al. Preservation of gene expression ratios among multiple complex cDNAs after PCR amplification: Application to differential gene expression studies. Journal of Structural and Functional Genomics. 2000, vol. 1, pp. 1-7.			
		KANAGAWA. Review: Bias and artifacts in multitemplate polymerase chain reactions (PCR). Journal of Bioscience and Bioengineering. 2003, vol. 96, no. 4, pp. 317-323.			
		LIU, et al. Inhibition of PCR amplification by a point mutation downstream of a primer. BioTechniques. 1997, vol. 22, no. 2, pp. 292-300.			
		LOCKHART, et al. Genomics, gene expression and DNA arrays. Nature. 2000, vol. 405, pp. 827-836.			
		LUEDERS, et al. Evaluation of PCR amplification bias by terminal restriction fragment length polymorphism analysis of small-subunit rRNA and mcrA genes by using defined template mixtures of methanogenic pure cultures and soil DNA extracts. Applied and Environmental Microbiology. 2003, vol. 69, no. 1, pp. 320-326.			
		MATHIEU-DAUDE, et al. DNA rehybridization during PCR: the 'C ₀ ' effect' and its consequences. Nucleic Acids Research. 1996, vol. 24, no. 11, pp. 2080-2086.			
↓		POLZ, et al. Bias in template-to-product ratios in multitemplate PCR. Applied and Environmental Microbiology. 1998, vol. 64, pp. 3724-3730.			
/KH/		SCHWABE, et al. High-copy cDNA amplification of minimal total RNA quantities for gene expression analyses. Molecular Biotechnology. 2000, vol. 14, pp. 165-172.			

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/KH/		SUZUKI, et al. Kinetic bias in estimates of coastal picoplankton community structure obtained by measurements of small-subunit rRNA gene PCR amplicon length heterogeneity. Applied and Environmental Microbiology. 1998, vol. 64, no. 11, pp. 4522-4529.				
		WADENBACK, et al. Comparison of standard exponential and linear techniques to amplify small cDNA samples for microarrays. BMC Genomics. 2005, vol. 6:61.				
		WAGNER, et al. Surveys of gene families using polymerase chain reaction: PCR selection and PCR drift. Systematic Biology. 1994, vol. 43, pp. 250-261.				
↓		WARNECKE, et al. Detection and measurement of PCR bias in quantitative methylation analysis of bisulphite-treated DNA. Nucleic Acids Research. 1997, vol. 25, no. 21, pp. 4422-4426				
/KH/		WINTZINGERODE, et al. Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiology Reviews. 1997, vol. 21, pp. 213-229.				

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